Amendments to the Specification

At the indicated page and line numbers, please replace the existing paragraphs with the ones set forth below.

(Page 7, line 29 through page 8, line 5)

(i) Novel, naturally occurring, nucleic acids, isolatable using the sequences of the present invention. They may include alleles (which will include polymorphisms or mutations at one or more bases - for instance *vrn1-1* (SEQ ID NO: 12) or *vrn1-2* (SEQ ID NO: 13) shown in Fig 7) or pseudoalleles (which may occur at closely linked loci to the VRN1 gene). Also included are paralogues, isogenes, or other homologous genes belonging to the same family as the VRN1 gene. Although these may occur at different genomic loci to the gene, they are likely to share conserved regions with it (see e.g. RTV1 in the Examples below). Also included are homologues of *VRN1* from other plant species.

(Page 36, lines 15-16)

Fig 6: Structure of the *VRN1* gene and transcript, and positions of the *vrn1-1* and *vrn1-2* mutations. SEQ ID NOs: 2 and 3 (top) and SEQ ID NOs: 4 and 5 (bottom) are shown in the nonsense mutation box and SEQ ID NOs: 6 and 7 (top) and SEQ ID NOs: 8 and 9 (bottom) are shown in the 1 bp deletion/frameshift mutation box.

(Page 36, lines 18-19)

Fig 7: The putative *VRN1* transcript and its deduced amino acid sequence (SEQ ID NO: 10; the amino acid sequence is SEQ ID NO: 11).

(Page 36, line 21)

Fig 8: Alignment of VRN1 (SEQ ID NO: 11) and RTV1 (SEQ ID NO: 48).

(Page 40, line 21 through page 41, line 14)
Eight cosmids (39K3, 8H8, 10F10, 42A10, 2P5, 19D3, 27J7, 67N6) centered around the marker agp14 were transformed into *vrn1-1 fca-1* plants by *Agrobacterium tumefaciens*-infection of root tissue (Hooykaas, 1989). In order to test if any of these cosmids rescued the mutant phenotype of *vrn1-1 fca-1*, T2 seed (from individual T1 kanamycin resistant transformants) was sown on soil and vernalized for 5 weeks. Seedlings were then transferred to LD conditions, and pricked out into individual compartments of divided trays after about a week of growth. The total leaf number prior to flowering was determined, and cosmids were scored as complementing if the segregation ratio of early to late plants (compared to *fca-1* and *vrn1-1 fca-1* controls) was approximately 3:1 or greater. Eight independent lines containing cosmid 8H8, eight independent lines containing cosmid 10F10, and three independent lines containing cosmid 39K3 were found to rescue mutant phenotype of *vrn1-1 fca-1*. Lines containing the other five cosmids did not complement the *vrn1-1* phenotype (Figure 3). Analysis of the flowering time segregation in typical 8H8 and 10F10 complementing lines is shown in Figure 4. The presence of each cosmid in complementing lines (T2 plants) was confirmed by a cosmid-specific diagnostic PCR, comprising an insert specific primer 8H8DIAG1 (ACCTGCTTCTGCCAACCGCTC; SEQ ID NO: 14) and 10F10DIAG1 (AGTTCGCTCTTGCTGTTTTTTTTCCC; SEQ ID NO: 15)(corresponding to a portion of the Ler genomic DNA) and a primer BACT 7U (CCTCTTCGCTATTACGCCAG; SEQ ID NO: 16) present in the cosmid vector (see "cosmid complementation" under "materials and methods" below).

(Page 55, lines 1-4)

BACT7U	5'- CCTCTTCGCTATTACGCCAG -3'	(SEQ ID NO: 16)
BACT7L	5'- GCCCTTCCCAACAGTTCG -3'	(SEQ ID NO: 17)
Sp6A	5'- CACACAGGAAACAGCTAT -3'	(SEQ ID NO: 18)
Sp6B	5'- ACACAACATACGAGCCGGAA -3'	(SEQ ID NO: 19)

(Page 60, lines 9-37)

Oligo	Strand	Position	Sequence (5' to 3')	
S63	+	850	CAACGGTTAGCCCAAAC	(SEQ ID NO: 20)
S64	-	866	GTTTGGGCTAACCGTTG	(SEQ ID NO: 21)
V11	+	1193	GAGACCAGTTTTGTTTTCC	(SEQ ID NO: 22)
S62	-	1229	GACAAATATAGGTGGAAAGG	(SEQ ID NO: 23)
S66	+	1441	AAAGGGGAGTAGGTGGG	(SEQ ID NO: 24)
V7	+	1811	CTCTCTGGTCTTCTCTTC	(SEQ ID NO: 25)
V10	-	1828	GAAGAGAAGACCAGAGAG	(SEQ ID NO: 26)
V6	+	1907	TTTTCTCATCCACTATCC	(SEQ ID NO: 27)
S51	-	1930	TTTCTTGGATAGTGGATGAG	(SEQ ID NO: 28)
S65	-	2166	AAAACAGGGAAGAGTAAGAAG	(SEQ ID NO: 29)
S52	+	2270	CATTGGTTGTGTTTGGTGGG	(SEQ ID NO: 30)
V5	+	2599	GGTCTCTATGTATTGTGC	(SEQ ID NO: 31)
V4	-	2616	GCACAATACATAGAGACC	(SEQ ID NO: 32)
V12	-	2846	AGATTGATTACACGACTCC	(SEQ ID NO: 33)
V8	+	3125	CCCAGATAAGTTTGTGAG	(SEQ ID NO: 34)
V3	+	3391	ATTCCGCTCACAACCAC	(SEQ ID NO: 35)
V15	-	3414	GTTTGAAGTGGTTGTGAG	(SEQ ID NO: 36)
V14	+	3477	TACCCATCACCACTTCC	(SEQ ID NO: 37)
S60	-	3474	CAGAAGAAGGAAAGATGACC	(SEQ ID NO: 38)
S61	+	3927	GAAGAAAGAGAGAGAGCC	(SEQ ID NO: 39)
V13	+	3976	ACCCTTTCTTCAGAGTG	(SEQ ID NO: 40)
V9	-	3942	CTCTCTCTCTTTCTTCTG	(SEQ ID NO: 41)
V16	-	3993	CCACTCTGAAGAAAGGG	(SEQ ID NO: 42)
S46	+	4096	CCTTCTGTTTCTGTTTCTC	(SEQ ID NO: 43)
S45	-	4114	GAGAAACAGAAACAGAAGG	(SEQ ID NO: 44)
V2	-	4431	AAGATACTCCTACACGAC	(SEQ ID NO: 45)
V17	+	4486	GTCTCGTTTTTTCTCTCGG	(SEQ ID NO: 46)
S49	-	4870	CTACCACAGTTCCCACCTAC	(SEQ ID NO: 47)

(Page 70, line 1)

Annex I - L*er* *VRN1* genomic (contig 29 [1501-6500]) (SEQ ID NO: 1)